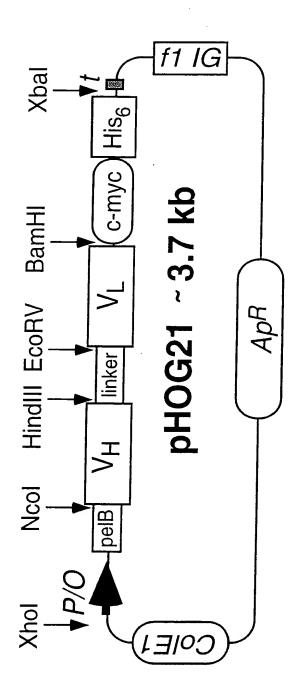
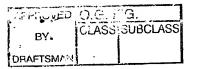
O.G. F.G. CLASSISUBCLASS

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EcoRI RBS PelB leader
131 GAATTCATTAAAGAGGAGAAATTAACCATGAAATACCTATTGCCTACGGCAGCCGCTGGCT
1▶ M K Y L L P T A A A G
Pstl
Ncol ♦ Pvull VH anti-CD3
192 TGCTGCTGCAGCTCAGCCGGCCATGGCGCAGGTGCAGCAGTCTGGGGCTGAA 12 L L L A A O P A M A O V O L O O S G A F
Frame-H1 254 CTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTACT <u>a G</u>
CDR-H1 Frame-H2
316 GTACACGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGA <u>TACA</u>
53 Y T M H W V K Q R P G Q G L E W I G Y
CDR-H2
375 TTAATCCTAGCCGTGGTTATACTAATTACAATCAGAAGTTCAAGGACAAGGCCA
73 FI N P S R G Y T N Y N Q K F K D K A
Frame-H3
429 CATTGACTACAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAG 91 T L T T D K S S S T A Y M O L S S L T S F
Pstl CDR-H3 491 GACTCTGCAGTCTATTACTGTGCAAGA <u>TATTATGATGATCATTACAGCCTTGACTAC</u>
112 D S A V Y Y C A R Y Y D D H Y S L D Y
Frame-H4 CH1 HindIII Yol linke
548 TGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAACACACCCAAGCTTGAAGAAGG
131 W G Q G T T L T V S S A K T T P K L E E G
EcoRV
Mlul VL anti-CD3 Frame-L1
Mlul VL anti-CD3 Frame-L1 610 <u>TGAATTTTCAGAAGCACGC</u> GTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT
Mlul VL anti-CD3 Frame-L1 610 <u>TGAATTTTCAGAAGCACGC</u> GTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151▶ E F S E A R V D I V L T Q S P A I M S A
Mlul VL anti-CD3 Frame-L1 610 <u>TGAATTTTCAGAAGCACGC</u> GTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151▶ E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCTGCTCACTTCAGGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3
MIUI VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTTATTACTGCCAGCAGTGGAGTAG
Mlul VL anti-CD3
MIUI VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCTGCTCACTTCAGGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCCACTTATTACTGCCAGCAGTTGGAGTAG 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa
Miul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTCCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGGCAGTGGGTCTGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAG 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa 907 TAACCCCATTCACGTTCGGGCTCGGGGCACAAGTTGGAAATAAACCGGGCTGATACTGCACC
Milui VL anti-CD3
MIUI VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAG 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa 907 TAACCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAACCGGGCTGATACTGCACC 250 N P F T F G S G T K L E I N R A D T A P BamHI c-myc epitope His6 tail
Milui VL anti-CD3
MILI VL anti-CD3 Frame-L1 610 TGAATTITCAGAAGCACCGCGTAGATATCGTGCTCACTCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A PSt! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGGCAGTGGGACTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAG 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa 907 TAACCCATTCACGTTCGGCTCGGGACAAAGTTGGAATAAACCGGGCTGATACTGCACC 250 N P F T F G S G T K L E I N R A D T A P BamHI c-myc epitope His6 tail 967 AACTGGATCCGAACAAAAGCTGATCTCAGGAGAAGAAGACCTTAAACTCACCATCACCATCACCATCC 270 T G S E Q K L I S E E D L N S H H H H H Xbal
Mili VL anti-CD3

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425 TOM OF TOTAL PROPERTY OF MAN 1999

EcoRI **RBS** PelB leader 1 GAATTCATTAAAGAGGAGAAATTAACCATGAAAATACCTATTGCCTACGGCAGCCGCTGGCTTGCTG 1 M K Y L L P T A A A G L L Ncol VH anti-CD3 Frame-H1 67 CTGCTGGCAGCTCAGCCGGCCATGGCGCAGGTGCAGCTGCAGCAGTCTGGGGGCTGAACTGGCAAGAC 14 LLAAQPAMAQVQLQQS GAELAR CDR-H1 134 CTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTACTAGGTACACGATGCA 36 P G A S V K M S C K A S G Y T F Y Frame-H2 CDR-H2 198 CTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATAAATCCTAGCCGTGG 57▶ W · V K Q R P G Q G L E W I G Y Ν Frame-H3 261 TTATACTAATTACAATCAGAAGTTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCA N Y N Q K F K D K A T L T T D K S S 323 GCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA<u>T</u>A 99 S T A Y M Q 1\ S S L T S E D S A V Y Y C A R CDR-H3 Frame-H4 390 TTATGATGATCATTACAGCCTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAG S /L D Y WGQGTTLTVSS CH1 Linker VL anti-CD19 452 CCAAAACAACACCCAAGCTTGGCGGTGATATCTTGCTCACCCAAACTCCAGCTTCTTTGGCTGTG DILLTQT K L G Ġ PASLAV CDR-L1 517 TCTCTAGGGCAGAGGGCCACCATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGA 164 S L G Q R A T I S C \ K A S Q S V Y Frame-L2 579 TAGTTATTTGAACTGGTACCAACAGATTCCAGGACAGCCACCCAAACTCCTCATCTATGATGCA 184▶ S Y N W Y Q Q I P G O P P K L L I CDR-L2 Frame-L3 643 TCCAATCTAGTTTCTGGGATCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCC N L V S G I P P R F S\G S G S G T D F T CDR-L3 707 TCAACATCCATCCTGTGGAGAAGGTGGATGCTGCAACCTAYCACTGTCAGCAAAGTACTGAGGA 227 L N I H P V E K V D A A T Y \H C Q S Frame-L4 C kappa Noti 771 <u>T</u>CCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA<u>CGGGCTGATGCT</u>GCGGCCGCTGGATCC PWTFGGGTKL E DAAAAGS I K c-myc epitope His6 tail BgIII 838 GAACAAAAGCTGATCTCAGAAGAAGACCTAAACTCA<u>CATCACCATCACCATCAC</u>TAAAGAT 271▶ E Ι S Ε E D L N S H H жннн 899 CT

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Balli **RBS** Pel B leader 1 AGATCTATTAAAGAGGAGAAATTAACCATGAAATACCTATTGCCTACGGCAGCCGCTGGCTTGC 1 M K Y L L P Т AAAGL VH anti-CD19 Frame-H1 TGCTGCTGGCAGCTCAGCCGGCCATGGCGCAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGT L A A Q PAMAQVQLO 0 S GAELV CDR-H1 129 GAGGCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTACTG PGSSVKISCKASGYAF Frame-H2 192 GATGAACIGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCT Ν V K Q R P G Q G L E W I G O ÒDR-H2 253 GGAGATGGTGÀTACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCA 76 G D G \mathbf{T} N Y N G K F KGKATL Frame-H3 310 GACGAATCCTCCAGCAÒAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTCTGCGGTCT S Т A Y M Q L S S L A S E D S A V E S S CDR-H3 374 ATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT 116 Y F C A R R E T TVGR Y Frame-H4 CH₁ Linker 431 <u>A.C</u>TGGGGTCAAGGAACCTCAGTCAGCGTCTCCTCAGCCAAAACAACACCC**AAGCTTGGCGGT** 135▶Y W G Q G T S V T\V S S A K T T P K VL anti-CD3 Frame-L1 493 GATATCGTGCTCACTCAGTCTCCAGCAA\CATGTCTGCATCTCCAGGGGAGAAGGTCACCATGA 156 DIVLTQSPAI\MSASPGE CDR-L1 Frame-L2 557 CCTGCAGTGCCAGCTCAAGTGTAAGTTACATGAACTGGTACCAGCAGAAGTCAGCCACC S V M N W Y O O K S G T S Y CDR-L2 616 TCCCCCAAAAGATGGATTTATGACACATCCAAA&TGGCTTCTGGAGTCCCTGCTCACTTC 197▶ S P K R W I Y K D T S Α S G V P Frame-L3 676 AGGGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCGGCATGGAGGCTGAAGATGCTG 217 R G S G S G T S Y S L T I S G M E A E D A CDR-L3 740 CCACTTATTACTGCCAGCAGTGGAGTAGTAACCCATTCACGTTCGGCTCGGGGACAAAG 238 A T Y Y C Q Q S S N Р F FGSGTK C kappa c-myc epitope 799 TTGGAAATAAACCGGGCTGATACTGCACCAACTGGATCCGAACAAAAGCTGATCTCAGAA TAPTGSE R A D Q ·Κ L His6 tail Xbal 859 GAAGACCTAAACTCACCATCACCATCACCATCACTAATCTAGA L N S ннннн

Fig. 3 (Fortsetzung)